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L2: Entry 3 of 3 File: USPT Oct 19, 1999

DOCUMENT-IDENTIFIER: US 5968744 A
TITLE: Human cornichon molecule

US Patent No. (1):
5968744

Detailed Description Text (59):
In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding CORN may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of CORN activity, it may be useful to encode a chimeric CORN protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the CORN encoding sequence and the heterologous protein sequence, so that CORN may be cleaved and purified away from the heterologous moiety.

Detailed Description Text (66):
In bacterial systems, a number of expression vectors may be selected depending upon the use intended for CORN. For example, when large quantities of CORN are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional E. coli cloning and expression vectors such as Bluescript.RTM. (Stratagene), in which the sequence encoding CORN may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

Detailed Description Text (81):
Host cells transformed with nucleotide sequences encoding CORN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CORN may be designed to contain signal sequences which direct secretion of CORN through a prokaryotic or eukaryotic cell membrane. Other constructions may be used to join sequences encoding CORN to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and CORN may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing CORN and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMAC (immobilized metal ion affinity chromatography as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3: 263-281) while the enterokinase cleavage site provides a means for purifying CORN from the fusion protein. A discussion of

vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; DNA Cell Biol. 12:441-453).

Detailed Description Text (194):
Induction of an isolated, transformed bacterial strain with IPTG using standard methods produces a fusion protein which consists of the first eight residues of .beta.-galactosidase, about 5 to 15 residues of linker, and the full length protein. The signal residues direct the secretion of CORN into the bacterial growth media which can be used directly in the following assay for activity.

L1: Entry 3 of 3 File: USPT Oct 19, 1999

DOCUMENT-IDENTIFIER: US 5968744 A
TITLE: Human cornichon molecule

US Patent No. (1):
5968744

Brief Summary Text (4):
Differentiation of tissues and determination of body plan in metazoans appears to be rooted in the synthesis of critical extracellular and intracellular proteins during oogenesis and embryogenesis. Determination of body plan is encrypted within embryonic cell lineages, and the fate of specific embryonic cell lineages is determined before fertilization, during oogenesis.

Brief Summary Text (5):
Oogenesis and embryogenesis are regulated by interactions between environmental, extracellular, and intracellular signals. Changes in signaling pathways caused by genetic mutation or biochemical modification can affect oogenesis and embryogenesis in a number of ways. Specifically, these changes may result in the failure of spermatozoa to fertilize the egg, in the premature death of the embryo, and in morphological changes during embryogenesis and during ontogeny.

Brief Summary Text (6):
Signaling pathways have been extensively studied during oogenes and embryogenesis of the fruit fly, Drosophila melanogaster. Soon after fertilization, the Drosophila embryo has two axes of polarity, the anterior-posterior axis and the dorsal-ventral axis. These axes of polarity have been observed in all other metazoan embryos thus far studied. The shape of the Drosophila egg shows dorsal-ventral polarity at the time it is laid. Genetic studies have shown that three sequential signaling pathways establish the dorsal-ventral axis in the Drosophila embryo. The first of these signaling pathways takes place during oogenesis, when the germline-derived oocyte is surrounded by an epithelium of somatically-derived follicle cells. The follicle cells later secrete components of the eggshell. The oocyte produces a dorsalizing signaling ligand that is received by receptors on neighboring follicle cells and defines the polarity of both the embryo and the eggshell. The proposed ligand and receptor in this pathway are encoded by the genes gurken and torpedo, which are members of the transforming growth factor-.alpha. and the epidermal growth factor-receptor families, respectively. Spatial localization of the signal is achieved by localizing gurken mRNA to the dorsal anterior side of the oocyte. This is proximal to the asymmetrically positioned dorsal-anterior-localized oocyte nucleus (Morisato, D. and Anderson, K. V. (1995) Annu. Rev. Genet. 29:371-399).

Brief Summary Text (7):
A number of other genes are also required to ensure correct dorsalization of the oocyte. One of the eight which has been identified is cornichon (Morisato and Anderson (supra)). The predicted cornichon translation product is a 144 amino acid residue hydrophobic protein. Hydrophobic residues are clustered at three distinct regions: the N-terminus, the central region, and the C-terminus of the molecule. There are no putative transmembrane or signal sequences (Roth, S. et al. (1995) Cell 81:967-978). cornichon is thought to be involved in the membrane localization or proper activation of the gurken protein (Morisato and Anderson, supra).

Detailed Description Text (55):
Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic

separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity may be converted to electrical signal using appropriate software (e.g. Genotype.TM. and Sequence Navigator.TM., Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample.

Detailed Description Text (72):
Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CORN. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding CORN, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) Results Probi. Cell Differ. 20:125-162).

Detailed Description Text (81):
Host cells transformed with nucleotide sequences encoding CORN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CORN may be designed to contain signal sequences which direct secretion of CORN through a prokaryotic or eukaryotic cell membrane. Other constructions may be used to join sequences encoding CORN to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and CORN may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing CORN and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMAC (immobilized metal ion affinity chromatography as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3: 263-281) while the enterokinase cleavage site provides a means for purifying CORN from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; DNA Cell Biol. 12:441-453).

Detailed Description Text (108):
As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5' or regulatory regions of the gene encoding CORN (signal sequence, promoters, enhancers, and introns). Oligonucleotides derived from the transcription initiation site, e.g., between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature (Gee, J. E. et al. (1994) In: Huber, B. E. and B. I. Carr, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, N.Y.). The complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Detailed Description Text (140):
In a particular aspect, the nucleotide sequences encoding CORN may be useful in assays that detect activation or induction of various cancers, particularly those mentioned above. The nucleotide sequences encoding CORN may be labeled by standard methods, and added to a fluid or tissue sample from a patient under conditions suitable for the

formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the biopsied or extracted sample is significantly altered from that of a comparable control sample, the nucleotide sequences have hybridized with nucleotide sequences in the sample, and the presence of altered levels of nucleotide sequences encoding CORN in the sample indicates the presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or in monitoring the treatment of an individual patient.

Detailed Description Text (186):
The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham, N.H.). Hybridization is carried out for 16 hours at 40.degree. C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1.times.saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR.TM. film (Kodak, Rochester, N.Y.) is exposed to the blots in a Phosphoimager cassette (Molecular Dynamics, Sunnyvale, Calif.) for several hours, hybridization patterns are compared visually.

Detailed Description Text (194):
Induction of an isolated, transformed bacterial strain with IPTG using standard methods produces a fusion protein which consists of the first eight residues of .beta.-galactosidase, about 5 to 15 residues of linker, and the full length protein. The signal residues direct the secretion of CORN into the bacterial growth media which can be used directly in the following assay for activity.

<first sequence: ss.P_AAZ11186 (length = 1033)
<second sequence: ss.DNA23330 (length = 1333)

<991 matches in an overlap of 999: 99.20 percent similarity
<gaps in first sequence: 0, gaps in second sequence: 0
<score: 2973 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

GenBank (Release 135, apr 2003)[May 6 11:28:38 2003]: 1 sequence found

P_AAZ11186 Gene encoding transmembrane domain containing protein clone HP02239. 033 bp, DNA, PAT 04-NOV-1999
ACCESSION P_AAZ11186
KEYWORDS Transmembrane domain containing protein; human; antibody production; interaction assay; diagnosis; nutritional activity; cytokine; cell proliferation; cell differentiation activity; immune stimulant; immune suppressant; haematopoiesis regulator; tissue growth activity; activin; inhibin activity; chemotaxis; chemokinesis; haemostasis; thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibitor; patent; GENESEQ patentdb.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1033)
AUTHORS Kato,S., Kimura,T., Nakamura,N., Sekine,S.
TITLE New proteins and DNA useful for preventing tumours
JOURNAL Patent: WO9943802-A2; Filing Date: 25-FEB-1999; 99WO-JP00875; Publication Date: 02-SEP-1999; Priority: 27-FEB-1998; 98JP-0046607; Assignee: (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM RES CENT; Cross Reference: WPI; 1999-527617/44. P-PSDB; AAY32925; Patent Format: Claim 4; Page 85-86; 96pp; English.
COMMENT This sequence encodes a human transmembrane protein of the invention. The DNAs are useful for expressing recombinant protein for analysis, characterisation or therapeutic use, and are useful as markers for tissues in which the corresponding protein is preferentially expressed. They are also useful as molecular weight markers on Southern gels, as chromosome markers or tags (when labelled) to identify potential genetic disorders, as probes to hybridise and thus discover novel, related DNA sequences, as a source of PCR primers for genetic fingerprinting, as probes to subtract-out known sequences in the process of discovering other novel DNAs, for selecting and making oligomers for attachment to a gene chip or other support, including for examination of expression patterns, to raise anti-protein antibodies using DNA immunisation techniques, and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the DNA encodes a protein which binds to another protein (e.g. in a receptor-ligand interaction), the DNA can also be used in interaction trap assays to identify DNAs encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The DNAs and proteins can have e.g. nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity.
FEATURES Location/Qualifiers

```
     CDS             48..482
                     /*tag=  a
                     /product= HP02239 protein
BASE COUNT      278 a    215 c    202 g    338 t
ORIGIN

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ss.P_AAZ11186   CTTTCTCCGCTGGCAACGGCGCCGCTCCCCGCTCCTCCTCCCCAGCCATGGCGTTCACGT
                                                          ** * *   * ************
ss.DNA23330                                           GCCCACGCGTCCGATGGCGTTCACGT
                                                            10        20

                           70        80        90       100       110       120
ss.P_AAZ11186   TCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCA
                ************************************************************
ss.DNA23330     TCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCA
                  30        40        50        60        70        80

                          130       140       150       160       170       180
ss.P_AAZ11186   TTTGGCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGT
                ************************************************************
ss.DNA23330     TTTGGCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGT
                  90        100       110       120       130       140

                          190       200       210       220       230       240
ss.P_AAZ11186   GTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCA
                ************************************************************
ss.DNA23330     GTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCA
                 150       160       170       180       190       200

                          250       260       270       280       290       300
ss.P_AAZ11186   TGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATC
                ************************************************************
ss.DNA23330     TGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATC
                 210       220       230       240       250       260

                          310       320       330       340       350       360
ss.P_AAZ11186   ATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAA
                ************************************************************
ss.DNA23330     ATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAA
                 270       280       290       300       310       320

                          370       380       390       400       410       420
ss.P_AAZ11186   CCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTT
                ************************************************************
ss.DNA23330     CCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTT
                 330       340       350       360       370       380

                          430       440       450       460       470       480
ss.P_AAZ11186   TTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTT
                ************************************************************
ss.DNA23330     TTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTT
                 390       400       410       420       430       440

                          490       500       510       520       530       540
ss.P_AAZ11186   AGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGG
                ************************************************************
ss.DNA23330     AGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGG
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                  450        460        470        480        490        500

                         550        560        570        580        590        600
ss.P_AAZ11186     GATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAA
                  ************************************************************
ss.DNA23330       GATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAA
                   510        520        530        540        550        560

                         610        620        630        640        650        660
ss.P_AAZ11186     AAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTGTTTTCA
                  ************************************************************
ss.DNA23330       AAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTGTTTTCA
                   570        580        590        600        610        620

                         670        680        690        700        710        720
ss.P_AAZ11186     TATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATGATT
                  ************************************************************
ss.DNA23330       TATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATGATT
                   630        640        650        660        670        680

                         730        740        750        760        770        780
ss.P_AAZ11186     ACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTGAA
                  ************************************************************
ss.DNA23330       ACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTGAA
                   690        700        710        720        730        740

                         790        800        810        820        830        840
ss.P_AAZ11186     TGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA
                  ************************************************************
ss.DNA23330       TGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA
                   750        760        770        780        790        800

                         850        860        870        880        890        900
ss.P_AAZ11186     GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGT
                  ************************************************************
ss.DNA23330       GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGT
                   810        820        830        840        850        860

                         910        920        930        940        950        960
ss.P_AAZ11186     GCTTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATC
                  ************************************************************
ss.DNA23330       GCTTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATC
                   870        880        890        900        910        920

                         970        980        990       1000       1010       1020
ss.P_AAZ11186     TGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCT
                  ************************************************************
ss.DNA23330       TGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCT
                   930        940        950        960        970        980

                        1030
ss.P_AAZ11186     TCGCTTGAATATT
                  *************
ss.DNA23330       TCGCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGA
                   990       1000       1010       1020       1030       1040

ss.DNA23330       GTAATAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGC
                  1050       1060       1070       1080       1090       1100
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ss.DNA23330     TGAATTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACA
                1110       1120       1130       1140       1150       1160

ss.DNA23330     TTACTTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCT
                1170       1180       1190       1200       1210       1220

ss.DNA23330     TAAGAATTTGCAGGTACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATC
                1230       1240       1250       1260       1270       1280

ss.DNA23330     CTGCTGTTCCTTTAGTGCAATACAATAAAACTCTGAAATTAAGACTC
                1290       1300       1310       1320       1330
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<first sequence: ss.P_AAX30168 (length = 1404)
<second sequence: ss.DNA23330 (length = 1333)

<1321 matches in an overlap of 1333: 99.10 percent similarity
<gaps in first sequence: 0, gaps in second sequence: 0
<score: 3963 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

P_AAX30168 Human secreted protein gene 24. 404 bp, DNA, PAT 18-JUN-1999
ACCESSION P_AAX30168
KEYWORDS Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; patent; GENESEQ patentdb.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Fan,P., Kyaw,H., Rosen,C.A., Ruben,S.M., Wei,Y.F.
TITLE New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
JOURNAL Patent: WO9910363-A1; Filing Date: 27-AUG-1998; 98WO-US17709; Publication Date: 04-MAR-1999; Priority: 29-AUG-1997; 97US-0056271. 29-AUG-1997; 97US-0056073. 29-AUG-1997; 97US-0056247. 29-AUG-1997; 97US-0056270; Assignee: (HUMA-) HUMAN GENOME SCI INC; Cross Reference: WPI; 1999-190585/16. P-PSDB; AAY04316; Patent Format: Claim 1; Page 145; 170pp; English.
COMMENT AAX30145 to AAX30173 represent 29 isolated human secreted protein genes. AAY04293 to AAY04321 represent the secreted proteins encoded by the 29 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences given in AAX30174 to AAX30182 and AAY04322 to AAY04334 are used in the exemplification of the present invention.
FEATURES Location/Qualifiers
BASE COUNT 418 a 263 c 260 g 462 t 1 others
ORIGIN

```
                    10        20        30        40        50        60
ss.P_AAX30168   GTGGATCCCCGGGCTGCAGGAATTCGGCAACGGCGXCCGCTCCCCGCTCCTCCTCCCCAG
                                                                  ** * *
ss.DNA23330                                                       GCCCACGCGTC
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                                                                    10

                    70         80         90        100        110        120
ss.P_AAX30168   CCATGGCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGC
                * ************************************************************
ss.DNA23330     CGATGGCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGC
                       20         30         40         50         60         70

                   130        140        150        160        170        180
ss.P_AAX30168   TCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGA
                ************************************************************
ss.DNA23330     TCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGA
                       80         90        100        110        120        130

                   190        200        210        220        230        240
ss.P_AAX30168   ATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACG
                ************************************************************
ss.DNA23330     ATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACG
                      140        150        160        170        180        190

                   250        260        270        280        290        300
ss.P_AAX30168   CTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGC
                ************************************************************
ss.DNA23330     CTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGC
                      200        210        220        230        240        250

                   310        320        330        340        350        360
ss.P_AAX30168   CCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGAC
                ************************************************************
ss.DNA23330     CCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGAC
                      260        270        280        290        300        310

                   370        380        390        400        410        420
ss.P_AAX30168   TCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGAT
                ************************************************************
ss.DNA23330     TCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGAT
                      320        330        340        350        360        370

                   430        440        450        460        470        480
ss.P_AAX30168   GGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATG
                ************************************************************
ss.DNA23330     GGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATG
                      380        390        400        410        420        430

                   490        500        510        520        530        540
ss.P_AAX30168   TTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAA
                ************************************************************
ss.DNA23330     TTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAA
                      440        450        460        470        480        490

                   550        560        570        580        590        600
ss.P_AAX30168   GCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCT
                ************************************************************
ss.DNA23330     GCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCT
                      500        510        520        530        540        550

                   610        620        630        640        650        660
ss.P_AAX30168   GATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTG
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                  ************************************************************
ss.DNA23330       GATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTG
                        560       570       580       590       600       610

                         670       680       690       700       710       720
ss.P_AAX30168     GAAAGACTGTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAT
                  ************************************************************
ss.DNA23330       GAAAGACTGTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAT
                        620       630       640       650       660       670

                         730       740       750       760       770       780
ss.P_AAX30168     TAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAG
                  ************************************************************
ss.DNA23330       TAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAG
                        680       690       700       710       720       730

                         790       800       810       820       830       840
ss.P_AAX30168     CCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGT
                  ************************************************************
ss.DNA23330       CCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGT
                        740       750       760       770       780       790

                         850       860       870       880       890       900
ss.P_AAX30168     TTATAGGAACTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAG
                  ************************************************************
ss.DNA23330       TTATAGGAACTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAG
                        800       810       820       830       840       850

                         910       920       930       940       950       960
ss.P_AAX30168     CTGTAGATATCAGGTGCTTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTC
                  ************************************************************
ss.DNA23330       CTGTAGATATCAGGTGCTTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTC
                        860       870       880       890       900       910

                         970       980       990      1000      1010      1020
ss.P_AAX30168     ATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAA
                  ************************************************************
ss.DNA23330       ATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAA
                        920       930       940       950       960       970

                        1030      1040      1050      1060      1070      1080
ss.P_AAX30168     GCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCC
                  ************************************************************
ss.DNA23330       GCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCC
                        980       990      1000      1010      1020      1030

                        1090      1100      1110      1120      1130      1140
ss.P_AAX30168     CATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGA
                  ************************************************************
ss.DNA23330       CATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGA
                       1040      1050      1060      1070      1080      1090

                        1150      1160      1170      1180      1190      1200
ss.P_AAX30168     TATAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTT
                  ************************************************************
ss.DNA23330       TATAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTT
                       1100      1110      1120      1130      1140      1150
```

```
                        1210       1220       1230       1240       1250       1260
ss.P_AAX30168    TTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGG
                 ************************************************************
ss.DNA23330      TTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGG
                      1160       1170       1180       1190       1200       1210

                        1270       1280       1290       1300       1310       1320
ss.P_AAX30168    TGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAAACTGAATGAGAGAA
                 ************************************************************
ss.DNA23330      TGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAAACTGAATGAGAGAA
                      1220       1230       1240       1250       1260       1270

                        1330       1340       1350       1360       1370       1380
ss.P_AAX30168    AATTGTATAACCATCCTGCTGTTCCTTTAGTGCAATACAATAAAACTCTGAAATTAACTC
                 ************************************************************ *
ss.DNA23330      AATTGTATAACCATCCTGCTGTTCCTTTAGTGCAATACAATAAAACTCTGAAATTAAGAC
                      1280       1290       1300       1310       1320       1330

                        1390       1400
ss.P_AAX30168    AAAAAAAAAAAAAAAAAACTCGTA

ss.DNA23330      TC
```

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<first sequence: ss.AA902726 (length = 500)
<second sequence: ss.DNA23330 (length = 1333)

<240 matches in an overlap of 500: 48.00 percent similarity
<gaps in first sequence: 6 (151 bases), gaps in second sequence: 1 (7 bases)
<score: 606 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

GenBank (Release 135, apr 2003)[May  6 09:17:26 2003]:

AA902726    ok71h07.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519453 3',
            mRNA sequence. 500 bp, mRNA, linear, EST 09-JUN-1998
ACCESSION   AA902726
VERSION     AA902726.1  GI:3037849
KEYWORDS    EST; NCI_est; 3_prime.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
REFERENCE   1  (bases 1 to 500)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     High quality stops: 375; insert: 1413.
FEATURES             Location/Qualifiers
     source          1..500
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1519453"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      180 a      81 c      66 g     173 t
ORIGIN

ss.DNA23330   GCCCACGCGTCCGATGGCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCT
                     10        20        30        40        50        60
ss.DNA23330   CACTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGAC
                     70        80        90       100       110       120
ss.DNA23330   TGATTACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTA
                    130       140       150       160       170       180
ss.DNA23330   CCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGG
                    190       200       210       220       230       240
ss.DNA23330   TCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAG
                    250       260       270       280       290       300
ss.DNA23330   TGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA
```

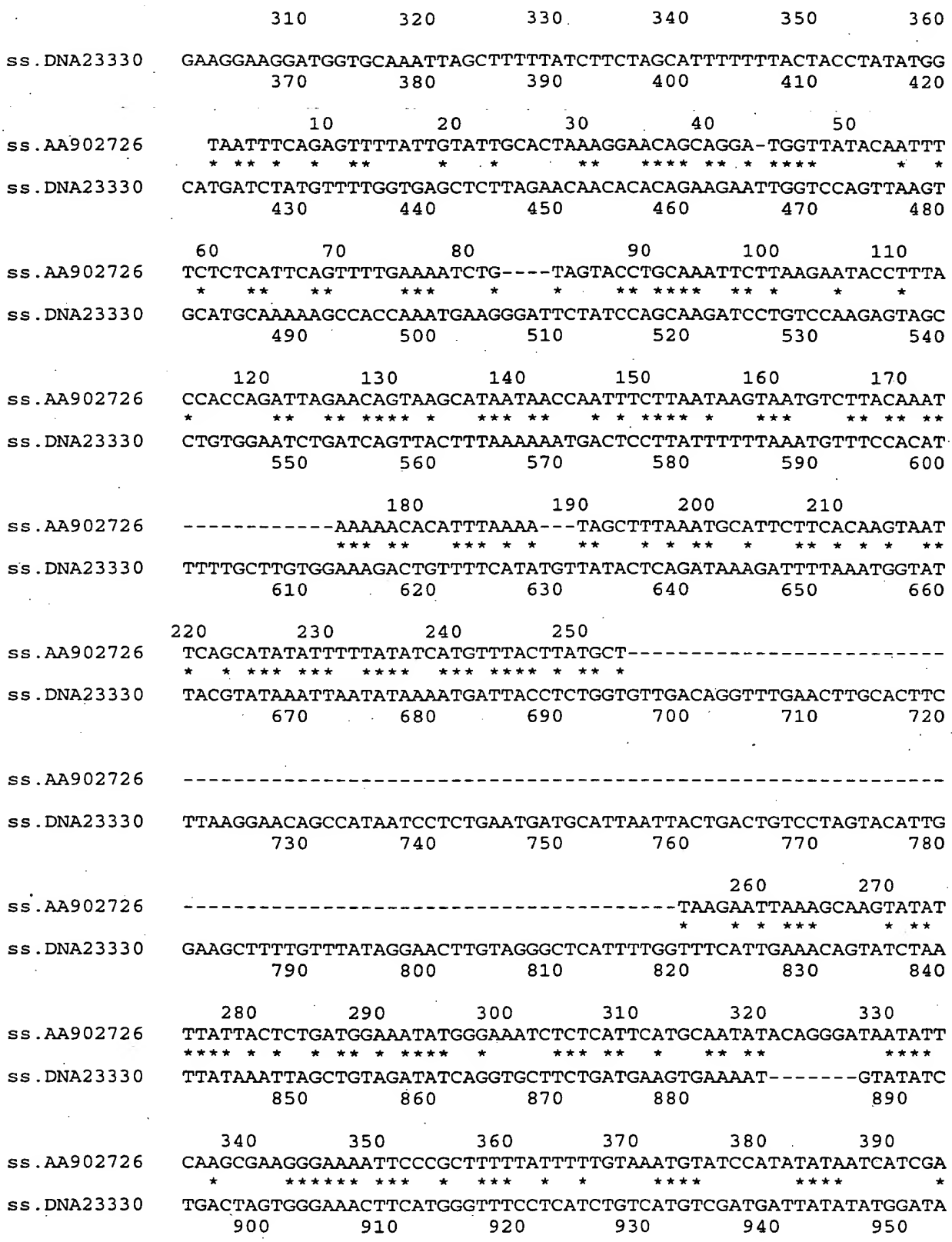
310 320 330 340 350 360
ss.DNA23330 GAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGG
370 380 390 400 410 420
10 20 30 40 50
ss.AA902726 TAATTTCAGAGTTTTATTGTATTGCACTAAAGGAACAGCAGGA-TGGTTATACAATTT
ss.DNA23330 CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGT
430 440 450 460 470 480
60 70 80 90 100 110
ss.AA902726 TCTCTCATTCAGTTTTGAAAATCTG----TAGTACCTGCAAATTCTTAAGAATACCTTTA
ss.DNA23330 GCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC
490 500 510 520 530 540
120 130 140 150 160 170
ss.AA902726 CCACCAGATTAGAACAGTAAGCATAATAACCAATTTCTTAATAAGTAATGTCTTACAAAT
ss.DNA23330 CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT
550 560 570 580 590 600
180 190 200 210
ss.AA902726 ----------AAAAACACATTTAAAA---TAGCTTTAAATGCATTCTTCACAAGTAAT
ss.DNA23330 TTTTGCTTGTGGAAAGACTGTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT
610 620 630 640 650 660
220 230 240 250
ss.AA902726 TCAGCATATATTTTTATATCATGTTTACTTATGCT-------------------------
ss.DNA23330 TACGTATAAATTAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTC
670 680 690 700 710 720
ss.AA902726 ----------
ss.DNA23330 TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG
730 740 750 760 770 780
260 270
ss.AA902726 ----------TAAGAATTAAAGCAAGTATAT
ss.DNA23330 GAAGCTTTTGTTTATAGGAACTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAA
790 800 810 820 830 840
280 290 300 310 320 330
ss.AA902726 TTATTACTCTGATGGAAATATGGGAAATCTCTCATTCATGCAATATACAGGGATAATATT
ss.DNA23330 TTATAAATTAGCTGTAGATATCAGGTGCTTCTGATGAAGTGAAAAT-------GTATATC
850 860 870 880 890
340 350 360 370 380 390
ss.AA902726 CAAGCGAAGGGAAAATTCCCGCTTTTTATTTTTGTAAATGTATCCATATATAATCATCGA
ss.DNA23330 TGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATA
900 910 920 930 940 950

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                   400        410        420        430                440
ss.AA902726    CATGACAGATGAGGAAACCCATGAAGTTTCCCACTAGTCAGATA-------TACATTTTC
               ***      *  *  ***  *  *** ******     *   ***        *  ** **
ss.DNA23330    CATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTG
                   960        970        980        990       1000       1010

               450        460        470        480       490        500
ss.AA902726    ACTTCATCAGAAGCACCTGATATCTACAGCTAATTTATAATTAGATACTGTTT
                 *  ** ***     *  **** * ** *  * * **** ** *     ***
ss.DNA23330    CATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTT
                  1020       1030       1040       1050      1060       1070

ss.DNA23330    AAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAA
                  1080       1090       1100       1110      1120       1130

ss.DNA23330    AGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATG
                  1140       1150       1160       1170      1180       1190

ss.DNA23330    CTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTT
                  1200       1210       1220       1230      1240       1250

ss.DNA23330    CAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCTTTAGTGCAATACAATA
                  1260       1270       1280       1290      1300       1310

ss.DNA23330    AAACTCTGAAATTAAGACTC
                  1320       1330
```

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<first sequence: ss.AA689524 (length = 544)
<second sequence: ss.DNA23330 (length = 1333)

<544 matches in an overlap of 544: 100.00 percent similarity
<gaps in first sequence: 1 (1 base), gaps in second sequence: 0
<score: 1623 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

GenBank (Release 135, apr 2003)[May  6 08:58:44 2003]:

AA689524    ns66e01.r1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1188600 5'
            similar to SW:CNI_DROME P49858 CORNICHON PROTEIN. ;, mRNA sequence.
            544 bp, mRNA, linear, EST 24-DEC-1997
ACCESSION   AA689524
VERSION     AA689524.1  GI:2689871
KEYWORDS    EST; NCI_est; 5_prime.
SOURCE      Homo sapiens (human).
  ORGANISM  Homo sapiens
REFERENCE   1  (bases 1 to 544)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     High quality stops: 499; insert: 484.
FEATURES             Location/Qualifiers
     source          1..544
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1188600"
                     /clone_lib="NCI_CGAP_Pr22"
                     /sex="male"
                     /tissue_type="normal prostate"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I  and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized, and was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      165 a     91 c    103 g    185 t
ORIGIN

ss.DNA23330   GCCCACGCGTCCGATGGCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCT
                     10        20        30        40        50        60

ss.DNA23330   CACTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGAC
                     70        80        90       100       110       120

ss.DNA23330   TGATTACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTA
                    130       140       150       160       170       180

ss.DNA23330   CCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGG
                    190       200       210       220       230       240


ss.AA689524                                                       GTGATGAG
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                                                                  ********
ss.DNA23330    TCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAG
                      250       260       270       280       290       300

               10        20        30        40        50        60
ss.AA689524    TGG-CCAGGACTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA
               *** ************************************************************
ss.DNA23330    TGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA
                      310       320       330       340       350       360

                70        80        90       100       110       120
ss.AA689524    GAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGG
               ************************************************************
ss.DNA23330    GAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGG
                      370       380       390       400       410       420

               130       140       150       160       170       180
ss.AA689524    CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGT
               ************************************************************
ss.DNA23330    CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGT
                      430       440       450       460       470       480

               190       200       210       220       230       240
ss.AA689524    GCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC
               ************************************************************
ss.DNA23330    GCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC
                      490       500       510       520       530       540

               250       260       270       280       290       300
ss.AA689524    CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT
               ************************************************************
ss.DNA23330    CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT
                      550       560       570       580       590       600

               310       320       330       340       350       360
ss.AA689524    TTTTGCTTGTGGAAAGACTGTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT
               ************************************************************
ss.DNA23330    TTTTGCTTGTGGAAAGACTGTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT
                      610       620       630       640       650       660

               370       380       390       400       410       420
ss.AA689524    TACGTATAAATTAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTC
               ************************************************************
ss.DNA23330    TACGTATAAATTAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTC
                      670       680       690       700       710       720

               430       440       450       460       470       480
ss.AA689524    TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG
               ************************************************************
ss.DNA23330    TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG
                      730       740       750       760       770       780

               490       500       510       520       530       540
ss.AA689524    GAAGCTTTTGTTTATAGGAACTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATC
               ************************************************************
ss.DNA23330    GAAGCTTTTGTTTATAGGAACTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAA
                      790       800       810       820       830       840
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ss.DNA23330    TTATAAATTAGCTGTAGATATCAGGTGCTTCTGATGAAGTGAAAATGTATATCTGACTAG
                     850        860        870        880        890        900

ss.DNA23330    TGGGAAACTTCATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATACATTTAC
                     910        920        930        940        950        960

ss.DNA23330    AAAAATAAAAAGCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTGCATGAAT
                     970        980        990       1000       1010       1020

ss.DNA23330    GAGAGATTTCCCATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATA
                    1030       1040       1050       1060       1070       1080

ss.DNA23330    AGTAAACATGATATAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATT
                    1090       1100       1110       1120       1130       1140

ss.DNA23330    TTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTG
                    1150       1160       1170       1180       1190       1200

ss.DNA23330    TTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAAACT
                    1210       1220       1230       1240       1250       1260

ss.DNA23330    GAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCTTTAGTGCAATACAATAAAACTCT
                    1270       1280       1290       1300       1310       1320

ss.DNA23330    GAAATTAAGACTC
                    1330
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<first sequence: ss.P_AAX90853 (length = 1378)
<second sequence: ss.DNA23330 (length = 1333)

<1325 matches in an overlap of 1333: 99.40 percent similarity
<gaps in first sequence: 0, gaps in second sequence: 0
<score: 3975 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

GenBank (Release 135, apr 2003)[May 6 11:26:58 2003]:

P_AAX90853 cDNA clone pk65_4. 378 bp, DNA, PAT 17-JAN-2000
ACCESSION P_AAX90853
KEYWORDS clone pk65_4; pk65_4 protein; human foetal kidney cDNA library; secreted protein; gene therapy; cytokine; nutritional activity; tissue growth; cell proliferation; immune stimulation; immune suppression; hematopoiesis regulation; tumour inhibition; patent; GENESEQ patentdb.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1378)
AUTHORS Jacobs,K., Mccoy,J.M., LaVallie,E.R., Collins-Racie,L.A., Evans,C. Merberg,D., Treacy,M., Agostino,M.J., Steininger,R.J.
TITLE Polynucleotides encoding secreted human proteins, derived from human adult brain, human fetal brain, human fetal kidney, and human adult blood cDNA libraries -
JOURNAL Patent: WO9950405-A1; Filing Date: 30-MAR-1999; 99WO-US06946; Publication Date: 07-OCT-1999; Priority: 31-MAR-1998; 98US-0080110. 29-MAR-1999; 99US-0280591; Assignee: (GEMY) GENETICS INST INC; Cross Reference: WPI; 1999-610849/52. P-PSDB; AAY28813; Patent Format: Claim 20; Page 104-105; 122pp; English.
COMMENT The present nucleotide sequence comprises the full-length protein-coding sequence of clone pk65_4. pk65_4 was isolated from a human foetal kidney cDNA library using methods specific for secreted protein cDNAs. This can be used in gene therapy. The polynucleotide and protein may effect nutritional activity, cytokine and cell proliferation, immune stimulation or suppression, hematopoiesis regulation, tissue growth, tumour inhibition etc.
FEATURES Location/Qualifiers
CDS 44..478
/*tag= a
/product= "pk65_4 protein"
BASE COUNT 411 a 258 c 252 g 457 t
ORIGIN

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                    10        20        30        40        50        60
ss.P_AAX90853   CTCCGCTGGCAACGGCGCCGCTCCCCGCTCCTCCTCCCCAGCCATGGCGTTCACGTTCGC
                                          ** * *   * ****************
ss.DNA23330                             GCCCACGCGTCCGATGGCGTTCACGTTCGC
                                                10        20        30

                    70        80        90       100       110       120
ss.P_AAX90853   GGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCATTTG
                ************************************************************
ss.DNA23330     GGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCATTTG
                        40        50        60        70        80        90

                   130       140       150       160       170       180
ss.P_AAX90853   GCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGTGTAA
```

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                  ************************************************************
ss.DNA23330       GCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGTGTAA
                         100       110       120       130       140       150

                         190       200       210       220       230       240
ss.P_AAX90853     TACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTT
                  ************************************************************
ss.DNA23330       TACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTT
                         160       170       180       190       200       210

                         250       260       270       280       290       300
ss.P_AAX90853     TCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATAT
                  ************************************************************
ss.DNA23330       TCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATAT
                         220       230       240       250       260       270

                         310       320       330       340       350       360
ss.P_AAX90853     TTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCAT
                  ************************************************************
ss.DNA23330       TTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCAT
                         280       290       300       310       320       330

                         370       380       390       400       410       420
ss.P_AAX90853     CATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTA
                  ************************************************************
ss.DNA23330       CATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTA
                         340       350       360       370       380       390

                         430       440       450       460       470       480
ss.P_AAX90853     TCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAA
                  ************************************************************
ss.DNA23330       TCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAA
                         400       410       420       430       440       450

                         490       500       510       520       530       540
ss.P_AAX90853     CAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATT
                  ************************************************************
ss.DNA23330       CAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATT
                         460       470       480       490       500       510

                         550       560       570       580       590       600
ss.P_AAX90853     CTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAA
                  ************************************************************
ss.DNA23330       CTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAA
                         520       530       540       550       560       570

                         610       620       630       640       650       660
ss.P_AAX90853     TGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTGTTTTCATATG
                  ************************************************************
ss.DNA23330       TGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTGTTTTCATATG
                         580       590       600       610       620       630

                         670       680       690       700       710       720
ss.P_AAX90853     TTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATGATTACCT
                  ************************************************************
ss.DNA23330       TTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATGATTACCT
                         640       650       660       670       680       690
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                    730        740        750        760        770        780
ss.P_AAX90853   CTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTGAATGAT
                ************************************************************
ss.DNA23330     CTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTGAATGAT
                    700        710        720        730        740        750

                    790        800        810        820        830        840
ss.P_AAX90853   GCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTAGGGC
                ************************************************************
ss.DNA23330     GCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTAGGGC
                    760        770        780        790        800        810

                    850        860        870        880        890        900
ss.P_AAX90853   TCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCTT
                ************************************************************
ss.DNA23330     TCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCTT
                    820        830        840        850        860        870

                    910        920        930        940        950        960
ss.P_AAX90853   CTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC
                ************************************************************
ss.DNA23330     CTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC
                    880        890        900        910        920        930

                    970        980        990       1000       1010       1020
ss.P_AAX90853   ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGC
                ************************************************************
ss.DNA23330     ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGC
                    940        950        960        970        980        990

                   1030       1040       1050       1060       1070       1080
ss.P_AAX90853   TTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAA
                ************************************************************
ss.DNA23330     TTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAA
                   1000       1010       1020       1030       1040       1050

                   1090       1100       1110       1120       1130       1140
ss.P_AAX90853   TAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAA
                ************************************************************
ss.DNA23330     TAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAA
                   1060       1070       1080       1090       1100       1110

                   1150       1160       1170       1180       1190       1200
ss.P_AAX90853   TTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTAC
                ************************************************************
ss.DNA23330     TTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTAC
                   1120       1130       1140       1150       1160       1170

                   1210       1220       1230       1240       1250       1260
ss.P_AAX90853   TTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAG
                ************************************************************
ss.DNA23330     TTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAG
                   1180       1190       1200       1210       1220       1230

                   1270       1280       1290       1300       1310       1320
ss.P_AAX90853   AATTTGCAGGTACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGC
                ************************************************************
ss.DNA23330     AATTTGCAGGTACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGC
```

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                    1240       1250       1260       1270       1280       1290

                    1330       1340       1350       1360       1370
ss.P_AAX90853   TGTTCCTTTAGTGCAATACAATAAAACTCTGAAATTAAGACTCAAAAAAAAAAAAAAA
                ****************************************
ss.DNA23330     TGTTCCTTTAGTGCAATACAATAAAACTCTGAAATTAAGACTC
                    1300       1310       1320       1330
```

L2 ANSWER 1 OF 1 MEDLINE on STN
AN 1999227056 MEDLINE
DN 99227056 PubMed ID: 10209299
TI The **human homolog** of **Drosophila cornichon** protein is differentially expressed in alloactivated T-cells.
AU Utku N; Bulwin G C; Beinke S; Heinemann T; Beato F; Randall J; Schnieders B; Sandhoff K; Volk H D; Milford E; Gullans S R
CS Institut fur Medizinische Immunologie, Campus Mitte, Charite, Humboldt Universitat, Schumannstrasse 20/21, 10098, Berlin, Germany.. nalan.utku@charite.de
NC DK36031 (NIDDK)
SO BIOCHIMICA ET BIOPHYSICA ACTA, (1999 Apr 1) 1449 (3) 203-10. Journal code: 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF022811; GENBANK-AF031379
EM 199905
ED Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990525
AB To identify novel genes induced in the early stage of T-cell activation, mRNA expression in alloactivated human lymphocytes was examined. Differential display-reverse transcription PCR analysis revealed a 207-bp cDNA fragment which was upregulated 24 h after allostimulation of a human T-cell line. The corresponding complete 1396 bp cDNA, named TGAM77, encodes a predicted 134 amino acid protein which shares 63% homology with the cornichon (cni) protein of Drosophila melanogaster. Upregulation of TGAM77 mRNA in the early phase of T-cell activation was confirmed by Northern blot and RT-PCR analysis of activated human lymphocytes. TGAM77 mRNA is expressed in a variety of human tissues with various expression levels. In analogy to cni which is involved in an epidermal growth factor-like signaling pathway inducing cellular asymmetry in Drosophila oogenesis, TGAM77 might function in similar signaling establishing vectorial re-localization and concentration of signaling events in T-cell activation.

L1 ANSWER 1 OF 1 MEDLINE on STN
AN 2001401135 MEDLINE
DN 21347415 PubMed ID: 11455434
TI **Isolation** of **genes involved** in **ascidian metamorphosis**: epidermal growth factor signaling and metamorphic competence.
AU Davidson B; Swalla B J
CS Zoology Department and Center for Developmental Biology, University of Washington, Box 351800, Seattle, WA 98195-1800, USA.
SO DEVELOPMENT GENES AND EVOLUTION, (2001 Apr) 211 (4) 190-4.
Journal code: 9613264. ISSN: 0949-944X.
CY Germany: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200110
ED Entered STN: 20011029
Last Updated on STN: 20011029
Entered Medline: 20011025
AB Although embryonic development in ascidians has been studied for over a century, the signals involved in coordinating post-larval development and metamorphosis are just beginning to be investigated. In this paper, we demonstrate that transcription is necessary for both the acquisition of metamorphic competence and the completion of the initial events of metamorphosis in Boltenia villosa. Transcripts expressed during metamorphic competence were isolated by a suppressive PCR subtraction of Boltenia villosa larval cDNAs. One of these transcripts is homologous to cornichon. Cornichon has a crucial but undefined role in epidermal growth factor (EGF) signaling during Drosophila embryogenesis. In situ hybridization demonstrates that Boltenia cornichon (Cnib) is expressed in the anterior papillary region of larvae as they gain competence. Our hypothesis is that Cnib acts to potentiate EGF signaling, thereby allowing Boltenia larvae to respond to cues for metamorphosis. Further research into the role of Cnib in urochordate metamorphosis may provide insight into the function of cornichon in other organisms. A better molecular understanding of urochordate metamorphosis will also provide a foundation for exploring the role of metamorphosis in chordate evolution.